AMENDMENT TO THE SPECIFICATION:

The specification has been amended as follows: Underlines indicate insertions and ~~strikethrough~~ indicate deletions.

Please replace the paragraph starting with "The present application" at page 1 with the following amended paragraph:

The present application is a continuation-in-part of application USSN 10/680,144 filed on October 8, 2003, ~~which is still pending~~ now abandoned and which is a continuation-in-part of application USSN 09/785,301 filed on February 20, 2001, ~~which is still pending~~ now abandoned and which claimsed the benefit of priority on provisional application USSN 60/184,343 filed on February 23, 2000, which applications are hereby incorporated by reference.

Please replace the paragraph starting with "Figure 1" at page 12 with the following amended paragraph:

Fig. 1 illustrates the primary structure of HOXB4. HOXB4 is a relatively small protein of 251 amino acids. Based on comparative analysis with paralogs and orthologs, the HOXB4 protein can be divided into 6 distinct domains. A: Foremost N-terminal domain: Conserved from *Drosophila* to human; B: Very little conservation; proline rich in human Hoxb4; c: Pbx-interacting hexapeptide; highly conserved from Drosophila to human; D: Region between hexapeptide and HD; highly conserved between vertebrate paralogs; E: homeodomain; highly conserved from *Drosophila* to human; and F: C-terminal domain.

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Please replace the paragraph starting with "Figure 7" at page 13 with the following amended paragraph:

Fig. 7 illustrates Biochemical properties of HOXB4 proteins. a) Schematic representation of TAT-HOXB4 protein also showing the TAT sequence of SEQ ID NO: 6. b) Purity of recombinant TAT-HOXB4 as detected on Coomasie blue-stained polyacrylamide gel.

BL, bacterial lysate; H, purified TAT-HOXB4. c) HOXB4 levels in 50,000 retrovirally transduced BM cells (lane 8) compared to various concentrations of TAT-HOXB4 (lanes 1-7). d TAT-HOXB4 enters the nuclear of Rat-1 cells. e) Stability of TAT-HOXB4 in medium containing 10% FSC. f) Pulse chase analyses suggesting that t1/2 of intracellular HOXB4 in hemopoietic cells is only ~1 hr.

Please replace the paragraph bridging pages 55 and 56 with the following amended paragraph:

C-kit$^+$ cells were purified from E14.5 fetal livers of Pep3b mice by fluorescence activated cell sorting (FACS) on a MoFlo instrument (Dako Cytomation Inc. Fort Collins, Co). Total RNA was isolated by Trizol ,™ DNase-I-treated and cDNA was prepared (MMLV-RT, random primers) according to the manufacturer's instructions (InVitrogen, Paisley U.K.). Q-PCR was carried out using TaqMan® probe based chemistry (Applera, Foster City, CA). Oligonucleotides for all 39 murine Hox genes were designed against nucleotide sequences deposited in murine genome databases (GenBank ~~www.psc.edu/general/software/packages/genbank/genbank.html,~~ ~~RefSeq www.ncbi.nlm.nih.gov/RefSeq/~~ and EMBL ~~www.ebi.ac.uk/embl/~~ using Primer Express™ (Applera). Reactions, analysis and validation of the Hox amplicons were carried out as previously described (Thompson et al 2003). The highest Hox expression observed (500 to 2000 copies) was completely restricted to the a cluster, consistent with previous findings (Sauvageau et al. PNAS, 1994) and only Hoxa13 was not expressed in these primitive cells. The low to moderately expressed elements (20 to 500 copies) included Hoxb and Hoxc cluster genes, with Hoxb4 being the highest expressed non-a cluster paralog. All copy numbers were corrected for equal loading using an internal control (18s rRNA PDAR™ Applera). Standard curves of copy number versus C_T values were constructed from serial dilutions (10^7 to 10 copies) of linearised target amplicon-containing plasmids. All standard curves, correlation coefficients, gradient and intercept values were generated using the sequence detection system associated software (version 1.7) in accordance with the manufacturer's instructions (User bulletin number #2 ~~http://docs.appliedbiosystems.com/pebiodocs/04303859.pdf~~). Copy numbers of less than twenty were regarded as being not significantly expressed. Q-PCR was

carried out using TaqMan® probe based chemistry essentially as previously described (Thompson et al. Blood, 2003) with murine Hox-specific oligonucleotides. Standard curves were generated from Hox amplicon-containing plasmids using approved protocols (User bulletin#2 Applera) and copy numbers were obtained for 50 ng RNA equivalents.